

CRF Errors Corrected by the STIC System Branch

2113 OIRK

Serial Number: 09/770,102A

CHF Processing Date: 2/26/2002
 Edited by: AC
 Verified by: AC (STIC staff)

ENTERED

#8

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: globally corrected misspelling of "position"

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/770,102A

DATE: 02/26/2002

TIME: 17:35:43

Input Set : N:\Crf3\02142002\I770102A.raw

Output Set: N:\CRF3\02262002\I770102A.raw

P5

1 <110> APPLICANT: Cyclacel
 2 <120> TITLE OF INVENTION: Compositions and Methods for Monitoring the
 3 Modification of Modification
 4 Dependent Binding Partner Polypeptides
 5 <130> FILE REFERENCE: 10069/1062
 C--> 6 <140> CURRENT APPLICATION NUMBER: US/09/770,102A
 7 <141> CURRENT FILING DATE: 2001-01-25
 8 <150> PRIOR APPLICATION NUMBER: US 60/179283
 9 <151> PRIOR FILING DATE: 2000-01-31
 10 <160> NUMBER OF SEQ ID NOS: 57
 11 <170> SOFTWARE: PatentIn version 3.1
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 17
 15 <212> TYPE: PRT
 16 <213> ORGANISM: Unknown
 17 <220> FEATURE:
 18 <223> OTHER INFORMATION: ADP-ribosylation domain
 19 <221> NAME/KEY: DOMAIN
 20 <222> LOCATION: (1)..(17)
 21 <223> OTHER INFORMATION: ADT-ribosylation site
 22 <400> SEQUENCE: 1
 23 Met Leu Cys Cys Met Arg Arg Thr Lys Gln Val Glu Lys Asn Asp Asp
 24 1 5 10 15
 25 Asp
 27 <210> SEQ ID NO: 2
 28 <211> LENGTH: 10
 29 <212> TYPE: PRT
 30 <213> ORGANISM: Unknown
 31 <220> FEATURE:
 32 <223> OTHER INFORMATION: ADP-ribosylation site
 33 <221> NAME/KEY: DOMAIN
 34 <222> LOCATION: (1)..(10)
 35 <223> OTHER INFORMATION: ADP-ribosylation site
 36 <400> SEQUENCE: 2
 37 Phe Lys Gln Arg Gln Thr Arg Gln Phe Lys
 38 1 5 10
 40 <210> SEQ ID NO: 3
 41 <211> LENGTH: 30
 42 <212> TYPE: PRT
 43 <213> ORGANISM: Unknown
 44 <220> FEATURE:
 45 <223> OTHER INFORMATION: ubiquitination site
 46 <221> NAME/KEY: DOMAIN

RAW SEQUENCE LISTING

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Input Set : N:\Crf3\02142002\I770102A.raw

Output Set: N:\CRF3\02262002\I770102A.raw

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47 <222> LOCATION: (1)..(30)
48 <223> OTHER INFORMATION: ubiquitination site
49 <400> SEQUENCE: 3
50      Met Phe Gln Ala Ala Glu Arg Pro Gln Glu Trp Ala Met Glu Gly Pro
51      1              5              10              15
52      Arg Asp Gly Leu Lys Lys Glu Arg Leu Leu Asp Asp Arg His
53      20              25              30
55 <210> SEQ ID NO: 4
56 <211> LENGTH: 21
57 <212> TYPE: PRT
58 <213> ORGANISM: Unknown
59 <220> FEATURE:
60 <223> OTHER INFORMATION: ubiquitination site
61 <221> NAME/KEY: DOMAIN
62 <222> LOCATION: (1)..(21)
63 <223> OTHER INFORMATION: ubiquitination site
64 <400> SEQUENCE: 4
65      His Gly Ser Gly Ala Trp Leu Leu Pro Val Ser Leu Val Lys Arg Lys
66      1              5              10              15
67      Thr Thr Leu Ala Pro
68      20
70 <210> SEQ ID NO: 5
71 <211> LENGTH: 10
72 <212> TYPE: PRT
73 <213> ORGANISM: Unknown
74 <220> FEATURE:
75 <223> OTHER INFORMATION: O-GlcNAc site
76 <221> NAME/KEY: DOMAIN
77 <222> LOCATION: (1)..(10)
78 <223> OTHER INFORMATION: O-GlcNAc site
79 <400> SEQUENCE: 5
80      Gly Thr Thr Ser Thr Ile Gln Thr Ala Pro
81      1              5              10
83 <210> SEQ ID NO: 6
84 <211> LENGTH: 12
85 <212> TYPE: PRT
86 <213> ORGANISM: Unknown
87 <220> FEATURE:
88 <223> OTHER INFORMATION: O-GlcNAc site
89 <221> NAME/KEY: DOMAIN
90 <222> LOCATION: (1)..(12)
91 <223> OTHER INFORMATION: O-GlcNAc site
92 <400> SEQUENCE: 6
93      Ser Ala Val Ser Ser Ala Asp Gly Thr Val Leu Lys
94      1              5              10
96 <210> SEQ ID NO: 7
97 <211> LENGTH: 18
98 <212> TYPE: PRT
99 <213> ORGANISM: Unknown

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DATE: 02/26/2002

TIME: 17:35:43

Input Set : N:\Crf3\02142002\I770102A.raw

Output Set: N:\CRF3\02262002\I770102A.raw

100 <220> FEATURE:
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 102 <221> NAME/KEY: DOMAIN
 103 <222> LOCATION: (1)..(18)
 104 <223> OTHER INFORMATION: O-GlcNAc site
 105 <400> SEQUENCE: 7
 106 Asp Ser Ser Thr Asp Leu Thr Gln Thr Ser Ser Ser Gly Thr Val Thr
 107 1 5 10 15
 108 Leu Pro
 110 <210> SEQ ID NO: 8
 111 <211> LENGTH: 12
 112 <212> TYPE: PRT
 113 <213> ORGANISM: Unknown
 114 <220> FEATURE:
 115 <223> OTHER INFORMATION: O-GlcNAc site
 116 <221> NAME/KEY: DOMAIN
 117 <222> LOCATION: (1)..(12)
 118 <223> OTHER INFORMATION: O-GlcNAc site
 119 <400> SEQUENCE: 8
 120 Met Ala Gly Gly Pro Ala Asp Thr Ser Asp Pro Leu
 121 1 5 10
 123 <210> SEQ ID NO: 9
 124 <211> LENGTH: 13
 125 <212> TYPE: PRT
 126 <213> ORGANISM: Unknown
 127 <220> FEATURE:
 128 <223> OTHER INFORMATION: O-GlcNAc site
 129 <221> NAME/KEY: DOMAIN
 130 <222> LOCATION: (1)..(13)
 131 <223> OTHER INFORMATION: O-GlcNAc site
 132 <400> SEQUENCE: 9
 133 Ala Gln Thr Ile Thr Ser Glu Thr Pro Ser Ser Thr Thr
 134 1 5 10
 136 <210> SEQ ID NO: 10
 137 <211> LENGTH: 8
 138 <212> TYPE: PRT
 139 <213> ORGANISM: Unknown
 140 <220> FEATURE:
 141 <223> OTHER INFORMATION: Consensus sequence
 142 <221> NAME/KEY: MISC_FEATURE
 143 <222> LOCATION: (1)..(8)
 144 <223> OTHER INFORMATION: Xaa at position 6 may be any amino acid
 145 <221> NAME/KEY: MISC_FEATURE
 146 <222> LOCATION: (1)..(8)
 147 <223> OTHER INFORMATION: Xaa at position 3 may be any amino acid
 148 <400> SEQUENCE: 10
 149 Arg Arg Xaa Arg Arg Xaa Ser Thr
 150 1 5
 152 <210> SEQ ID NO: 11

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/770,102A

DATE: 02/26/2002

TIME: 17:35:43

Input Set : N:\Crf3\02142002\I770102A.raw

Output Set: N:\CRF3\02262002\I770102A.raw

153 <211> LENGTH: 5
 154 <212> TYPE: PRT
 155 <213> ORGANISM: Unknown
 156 <220> FEATURE:
 157 <223> OTHER INFORMATION: Consensus sequence
 158 <221> NAME/KEY: DOMAIN
 159 <222> LOCATION: (1)..(5)
 160 <223> OTHER INFORMATION: Consensus sequence, each Xaa is any amino acid
 161 <221> NAME/KEY: MISC_FEATURE
 162 <222> LOCATION: (1)..(5)
 163 <223> OTHER INFORMATION: X at position 2, 3, and 5 can be any amino acid
 164 <400> SEQUENCE: 11
 165 Lys Xaa Xaa Ser Xaa
 166 1 5
 168 <210> SEQ ID NO: 12
 169 <211> LENGTH: 3
 170 <212> TYPE: PRT
 171 <213> ORGANISM: Unknown
 172 <220> FEATURE:
 173 <223> OTHER INFORMATION: Consensus sequence
 174 <221> NAME/KEY: DOMAIN
 175 <222> LOCATION: (1)..(3)
 176 <223> OTHER INFORMATION: Consensus sequence, Xaa is any amino acid
 177 <221> NAME/KEY: MISC_FEATURE
 178 <222> LOCATION: (1)..(3)
 179 <223> OTHER INFORMATION: X at position 2 can be any amino acid
 180 <400> SEQUENCE: 12
 181 Arg Xaa Thr
 182 1
 184 <210> SEQ ID NO: 13
 185 <211> LENGTH: 5
 186 <212> TYPE: PRT
 187 <213> ORGANISM: Unknown
 188 <220> FEATURE:
 189 <223> OTHER INFORMATION: Consensus sequence
 190 <221> NAME/KEY: DOMAIN
 191 <222> LOCATION: (1)..(5)
 192 <223> OTHER INFORMATION: Consensus sequence, each Xaa is any amino acid
 193 <221> NAME/KEY: MISC_FEATURE
 194 <222> LOCATION: (1)..(5)
 195 <223> OTHER INFORMATION: X at position 2, 3, and 5 can be any amino acid
 196 <400> SEQUENCE: 13
 197 Arg Xaa Xaa Ser Xaa
 198 1 5
 200 <210> SEQ ID NO: 14
 201 <211> LENGTH: 4
 202 <212> TYPE: PRT
 203 <213> ORGANISM: Unknown
 204 <220> FEATURE:

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/770,102A

DATE: 02/26/2002

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Input Set : N:\Crf3\02142002\I770102A.raw

Output Set: N:\CRF3\02262002\I770102A.raw

205 <223> OTHER INFORMATION: Consensus sequence
 206 <221> NAME/KEY: DOMAIN
 207 <222> LOCATION: (1)..(4)
 208 <223> OTHER INFORMATION: Consensus sequence, each Xaa is any amino acid
 209 <221> NAME/KEY: MISC_FEATURE
 210 <222> LOCATION: (1)..(4)
 211 <223> OTHER INFORMATION: X at position 1 and 4 can be any amino acid
 212 <400> SEQUENCE: 14
 213 Xaa Ser Arg Xaa
 214 1
 216 <210> SEQ ID NO: 15
 217 <211> LENGTH: 8
 218 <212> TYPE: PRT
 219 <213> ORGANISM: Unknown
 220 <220> FEATURE:
 221 <223> OTHER INFORMATION: Consensus sequence
 222 <221> NAME/KEY: DOMAIN
 223 <222> LOCATION: (1)..(8)
 224 <223> OTHER INFORMATION: Consensus sequence, each Xaa is any amino acid
 225 <221> NAME/KEY: MISC_FEATURE
 226 <222> LOCATION: (1)..(8)
 227 <223> OTHER INFORMATION: X at position 1, 3, 4, 6 and 8 can be any amino acid
 228 <400> SEQUENCE: 15
 229 Xaa Arg Xaa Xaa Ser Xaa Arg Xaa
 230 1 5
 232 <210> SEQ ID NO: 16
 233 <211> LENGTH: 6
 234 <212> TYPE: PRT
 235 <213> ORGANISM: Unknown
 236 <220> FEATURE:
 237 <223> OTHER INFORMATION: Consensus sequence
 238 <221> NAME/KEY: DOMAIN
 239 <222> LOCATION: (1)..(6)
 240 <223> OTHER INFORMATION: Consensus sequence, each Xaa is any amino acid
 241 <221> NAME/KEY: MISC_FEATURE
 242 <222> LOCATION: (1)..(6)
 243 <223> OTHER INFORMATION: X at position 1, 3, 4, and 6 can be any amino acid
 244 <400> SEQUENCE: 16
 245 Xaa Arg Xaa Xaa Ser Xaa
 246 1 5
 248 <210> SEQ ID NO: 17
 249 <211> LENGTH: 6
 250 <212> TYPE: PRT
 251 <213> ORGANISM: Unknown
 252 <220> FEATURE:
 253 <223> OTHER INFORMATION: Consensus sequence
 254 <221> NAME/KEY: DOMAIN
 255 <222> LOCATION: (1)..(6)
 256 <223> OTHER INFORMATION: Consensus sequence

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/770,102A

DATE: 02/26/2002

TIME: 17:35:44

Input Set : N:\Crf3\02142002\I770102A.raw

Output Set: N:\CRF3\02262002\I770102A.raw

L:6 M:270 C: Current Application Number differs, Wrong Format
L:149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:197 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:213 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:290 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:306 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:696 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:712 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:728 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:744 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:760 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52